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RAW SEQUENCE LISTING   DATE: 12/12/2002
PATENT APPLICATION: US/10/010,160   TIME: 10:50:52

        Input Set : A:\SEQLIST DAVI110.001AUS.TXT
        Output Set: N:\CRF4\12122002\J010160.raw

 4 <110> APPLICANT: Rosey, Everett L.
 5   Strugnell, Richard A.
 6   Good, Robert T,
 7   King, Kendall W.
 9 <120> TITLE OF INVENTION: NOVEL THERAPEUTIC COMPOSITIONS FOR
10   TREATING INFECTION BY LAWSONIA SPP.
13 <130> FILE REFERENCE: DAVI110.001AUS
15 <140> CURRENT APPLICATION NUMBER: US 10/010,160
16 <141> CURRENT FILING DATE: 2001-11-09
18 <150> PRIOR APPLICATION NUMBER: AU PR1381
19 <151> PRIOR FILING DATE: 2000-11-10
21 <150> PRIOR APPLICATION NUMBER: US 60/249,596
22 <151> PRIOR FILING DATE: 2000-11-17
24 <160> NUMBER OF SEQ ID NOS: 68
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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29 <211> LENGTH: 622
30 <212> TYPE: DNA
31 <213> ORGANISM: Lawsonia intracellularis
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34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)...(621)
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42 cag gaa gct cgt tct gaa ggg agt gtc cct aaa tca gaa gag gtt act   96
43 Gln Glu Ala Arg Ser Glu Gly Ser Val Pro Lys Ser Glu Glu Val Thr
44   20   25   30
46 aaa gca ttg act act gca gca ggg atg ctg ggg ctt gct att tat tca   144
47 Lys Ala Leu Thr Thr Ala Ala Gly Met Leu Gly Leu Ala Ile Tyr Ser
48   35   40   45
50 ggc gta atg gga cgt cat ttt gaa aca att ttc tac tat att ttt aca   192
51 Gly Val Met Gly Arg His Phe Glu Thr Ile Phe Tyr Tyr Ile Phe Thr
52   50   55   60
54 gaa tca ttt cgg ttt gag gtt aca gca cag tca gta tat gct tta ttt   240
55 Glu Ser Phe Arg Phe Glu Val Thr Ala Gln Ser Val Tyr Ala Leu Phe
56 65   70   75   80
58 att tat gtt gct caa gag ata gct att tta ttg atg cca ata tta ctt   288
59 Ile Tyr Val Ala Gln Glu Ile Ala Ile Leu Leu Met Pro Ile Leu Leu
60   85   90   95
62 ttt att gct gtt acg gca tgg att tca tta cgt gta caa gtt ggt gca   336
63 Phe Ile Ala Val Thr Ala Trp Ile Ser Leu Arg Val Gln Val Gly Ala

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Input Set : A:\SEQLIST DAVI110.001AUS.TXT
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64            100                 105                  110
66 tta tgg act aca aag gtt ttt aaa ttt aaa tgg agt aaa ttt aat ata    384
67 Leu Trp Thr Thr Lys Val Phe Lys Phe Lys Trp Ser Lys Phe Asn Ile
68            115                 120                  125
70 ata aaa ggg ttg aaa gga atg ttt gct tct caa caa aca ctt gtt cga    432
71 Ile Lys Gly Leu Lys Gly Met Phe Ala Ser Gln Gln Thr Leu Val Arg
72     130                 135                 140
74 ctt tta cgt agt tta gtt caa gta att gtt ata ggt att gtt cca tat    480
75 Leu Leu Arg Ser Leu Val Gln Val Ile Val Ile Gly Ile Val Pro Tyr
76 145                 150                 155                  160
78 atg att ata aaa gga gag ttt tca aac ttt tta cca tta tat tat gca    528
79 Met Ile Ile Lys Gly Glu Phe Ser Asn Phe Leu Pro Leu Tyr Tyr Ala
80                 165                 170                  175
82 agt cct tca ggt gtg gca gat tat atg ctt aat aca gga ata gta ctt    576
83 Ser Pro Ser Gly Val Ala Asp Tyr Met Leu Asn Thr Gly Ile Val Leu
84            180                 185                  190
86 gtt tta tat acg cta att cct atg aca att att gca gtc gca gat        621
87 Val Leu Tyr Thr Leu Ile Pro Met Thr Ile Ile Ala Val Ala Asp
88            195                 200                  205
90 c                                                                  622
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92 <210> SEQ ID NO: 2
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94 <212> TYPE: PRT
95 <213> ORGANISM: Lawsonia intracellularis
97 <400> SEQUENCE: 2

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102 Lys Ala Leu Thr Thr Ala Ala Gly Met Leu Gly Leu Ala Ile Tyr Ser
103          35                 40                  45
104 Gly Val Met Gly Arg His Phe Glu Thr Ile Phe Tyr Tyr Ile Phe Thr
105     50                 55                  60
106 Glu Ser Phe Arg Phe Glu Val Thr Ala Gln Ser Val Tyr Ala Leu Phe
107 65                 70                 75                  80
108 Ile Tyr Val Ala Gln Glu Ile Ala Ile Leu Leu Met Pro Ile Leu Leu
109              85                 90                  95
110 Phe Ile Ala Val Thr Ala Trp Ile Ser Leu Arg Val Gln Val Gly Ala
111          100                105                  110
112 Leu Trp Thr Thr Lys Val Phe Lys Phe Lys Trp Ser Lys Phe Asn Ile
113          115                120                  125
114 Ile Lys Gly Leu Lys Gly Met Phe Ala Ser Gln Gln Thr Leu Val Arg
115     130                 135                 140
116 Leu Leu Arg Ser Leu Val Gln Val Ile Val Ile Gly Ile·Val Pro Tyr
117 145                 150                 155                  160
118 Met Ile Ile Lys Gly Glu Phe Ser Asn Phe Leu Pro Leu Tyr Tyr Ala
119              165                170                  175
120 Ser Pro Ser Gly Val Ala Asp Tyr Met Leu Asn Thr Gly Ile Val Leu
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131 <220> FEATURE:
132 <221> NAME/KEY: CDS
133 <222> LOCATION: (1)...(786)
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138 1               5                  10                  15
140 aca ttt tta cgt att agt gtt gtc tta ttt atg ctt cct ttt ttt tct    96
141 Thr Phe Leu Arg Ile Ser Val Val Leu Phe Met Leu Pro Phe Phe Ser
142             20                  25                  30
144 att gat ggt ttt cct aat atg tta aaa gca tca ata gct ctt att cta   144
145 Ile Asp Gly Phe Pro Asn Met Leu Lys Ala Ser Ile Ala Leu Ile Leu
146          35                  40                  45
148 act ata gtt ctt tgg ggg cgt ctt tct ctt tca gga aca caa atg cca   192
149 Thr Ile Val Leu Trp Gly Arg Leu Ser Leu Ser Gly Thr Gln Met Pro
150       50                  55                  60
152 gcg cat cct ttc gat cta gta ttg tta atc ata agc gag gtt ttt ctt   240
153 Ala His Pro Phe Asp Leu Val Leu Leu Ile Ile Ser Glu Val Phe Leu
154 65                  70                  75                  80
156 ggt att gta ttg ggg ctt gcg gta aac ttt ttc ttt gca gga att caa   288
157 Gly Ile Val Leu Gly Leu Ala Val Asn Phe Phe Phe Ala Gly Ile Gln
158                  85                  90                  95
160 gct ggg gga gaa att ctt gct aca caa atg ggg ttt aca atg att acg   336
161 Ala Gly Gly Glu Ile Leu Ala Thr Gln Met Gly Phe Thr Met Ile Thr
162             100                 105                 110
164 ctt gca gac cca tta act ggt aac acc aca ggt ttt att gca cat ttt   384
165 Leu Ala Asp Pro Leu Thr Gly Asn Thr Thr Gly Phe Ile Ala His Phe
166          115                 120                 125
168 ctt tat atg gtt gct aca tta gtt ttt ctt gct ctt aat ggc cat ttg   432
169 Leu Tyr Met Val Ala Thr Leu Val Phe Leu Ala Leu Asn Gly His Leu
170       130                 135                 140
172 ttt ctt ata aaa gct ttt aca tat act ttt aaa atg gtt cca gca gga   480
173 Phe Leu Ile Lys Ala Phe Thr Tyr Thr Phe Lys Met Val Pro Ala Gly
174 145                 150                 155                 160
176 gga ctt gtt gta aga gaa att tta ttg agt gaa ctt ctt aat atg gca   528
177 Gly Leu Val Val Arg Glu Ile Leu Leu Ser Glu Leu Leu Asn Met Ala
178                 165                 170                 175
180 ggg atg att ttt gtt ttt gcc tta cat gtt gcg gca cca gtt atg tca   576
181 Gly Met Ile Phe Val Phe Ala Leu His Val Ala Ala Pro Val Met Ser
182             180                 185                 190
184 gct ctt ttt tta gta gag atc tct tta gga ctt atg gca aga gct gct   624
185 Ala Leu Phe Leu Val Glu Ile Ser Leu Gly Leu Met Ala Arg Ala Ala
186          195                 200                 205
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188 cct cag att cat att atg gaa gtt gga ttt cct gta aaa att ggt gta    672
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190     210                 215                 220
192 gga ttt ttt ttc att gga cta tta ttt act atc tta tca aaa gaa acc    720
193 Gly Phe Phe Phe Ile Gly Leu Leu Phe Thr Ile Leu Ser Lys Glu Thr
194 225                 230                 235                 240
196 tat cga ttt att gca ggc cta gag gga cta ttt ttt aac tta ctt act    768
197 Tyr Arg Phe Ile Ala Gly Leu Glu Gly Leu Phe Phe Asn Leu Leu Thr
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201 Val Met Gly Ser Gly Lys
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206 <211> LENGTH: 262
207 <212> TYPE: PRT
208 <213> ORGANISM: Lawsonia intracellularis
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214             20                  25                  30
215 Ile Asp Gly Phe Pro Asn Met Leu Lys Ala Ser Ile Ala Leu Ile Leu
216         35                  40                  45
217 Thr Ile Val Leu Trp Gly Arg Leu Ser Leu Ser Gly Thr Gln Met Pro
218     50                  55                  60
219 Ala His Pro Phe Asp Leu Val Leu Leu Ile Ile Ser Glu Val Phe Leu
220 65                  70                  75                  80
221 Gly Ile Val Leu Gly Leu Ala Val Asn Phe Phe Phe Ala Gly Ile Gln
222                 85                  90                  95
223 Ala Gly Gly Glu Ile Leu Ala Thr Gln Met Gly Phe Thr Met Ile Thr
224                 100                 105                 110
225 Leu Ala Asp Pro Leu Thr Gly Asn Thr Thr Gly Phe Ile Ala His Phe
226         115                 120                 125
227 Leu Tyr Met Val Ala Thr Leu Val Phe Leu Ala Leu Asn Gly His Leu
228     130                 135                 140
229 Phe Leu Ile Lys Ala Phe Thr Tyr Thr Phe Lys Met Val Pro Ala Gly
230 145                 150                 155                 160
231 Gly Leu Val Val Arg Glu Ile Leu Leu Ser Glu Leu Leu Asn Met Ala
232                 165                 170                 175
233 Gly Met Ile Phe Val Phe Ala Leu His Val Ala Ala Pro Val Met Ser
234                 180                 185                 190
235 Ala Leu Phe Leu Val Glu Ile Ser Leu Gly Leu Met Ala Arg Ala Ala
236             195                 200                 205
237 Pro Gln Ile His Ile Met Glu Val Gly Phe Pro Val Lys Ile Gly Val
238     210                 215                 220
239 Gly Phe Phe Phe Ile Gly Leu Leu Phe Thr Ile Leu Ser Lys Glu Thr
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261  tca ttg aaa gga att ttt gaa gat gag ggc cat gaa gtt tta gaa aga    96
262  Ser Leu Lys Gly Ile Phe Glu Asp Glu Gly His Glu Val Leu Glu Arg
263              20                  25                  30
265  gct tca gca gaa gaa gga ctt aag tgt gtt gat gta gag tct cca gat   144
266  Ala Ser Ala Glu Glu Gly Leu Lys Cys Val Asp Val Glu Ser Pro Asp
267              35                  40                  45
269  ctt gtt ttt ctt gat att tgg ctt cct ggg atg gat ggt ctt atg gct   192
270  Leu Val Phe Leu Asp Ile Trp Leu Pro Gly Met Asp Gly Leu Met Ala
271          50                  55                  60
273  tta gac cat att cag gct ctt cat cag gaa tta cct gtt att atg att   240
274  Leu Asp His Ile Gln Ala Leu His Gln Glu Leu Pro Val Ile Met Ile
275      65                  70                  75                  80
277  tca ggt cat gcc aca att gaa act gct gta aca gct atc cgt caa ggt   288
278  Ser Gly His Ala Thr Ile Glu Thr Ala Val Thr Ala Ile Arg Gln Gly
279                  85                  90                  95
281  gct tat gat ttt att gaa aag cct ctt tct ttg gaa aaa gtc ctt att   336
282  Ala Tyr Asp Phe Ile Glu Lys Pro Leu Ser Leu Glu Lys Val Leu Ile
283              100                 105                 110
285  aca gct aat aga gct ata gaa aca gta aga tta aga agg gaa aac aaa   384
286  Thr Ala Asn Arg Ala Ile Glu Thr Val Arg Leu Arg Arg Glu Asn Lys
287          115                 120                 125
289  tta cta cgt act gta tta cct gag gag agt gag ttt ata gga cag tct   432
290  Leu Leu Arg Thr Val Leu Pro Glu Glu Ser Glu Phe Ile Gly Gln Ser
291      130                 135                 140
293  cct gtt atc tta aaa ttt aaa agt tta tta tca cag gtc gct cca aca   480
294  Pro Val Ile Leu Lys Phe Lys Ser Leu Leu Ser Gln Val Ala Pro Thr
295  145                 150                 155                 160
297  gat gct tgg gta cta ctt aca gga gag aat ggt aca ggt aaa gag tta   528
298  Asp Ala Trp Val Leu Leu Thr Gly Glu Asn Gly Thr Gly Lys Glu Leu
299                  165                 170                 175
301  gct gca caa gca ttg cac aaa gga agc tca cga tat caa aaa cca ttt   576
302  Ala Ala Gln Ala Leu His Lys Gly Ser Ser Arg Tyr Gln Lys Pro Phe
303              180                 185                 190
305  ata gct gtt aat tgt gct gct atc cct gaa gaa ttg att gaa agc gaa   624
306  Ile Ala Val Asn Cys Ala Ala Ile Pro Glu Glu Leu Ile Glu Ser Glu
307              195                 200                 205
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VERIFICATION SUMMARY   DATE: 12/12/2002
PATENT APPLICATION: **US/10/010,160**   TIME: 10:50:53

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